

Amendments to the Specification

Please replace the last full paragraph on page 88 with the following:

The number of nucleotide and protein sequences available in database systems has been growing exponentially for years. For example, the complete nucleotide sequences of *Caenorhabditis elegans* and several bacterial genomes, including *E. coli*, *Aeropyrum pernix*, *Aquifex aeolicus*, *Archaeoglobus fulgidus*, *Bacillus subtilis*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium tetani*, *Corynebacterium diphtheria*, *Deinococcus radiodurans*, *Haemophilus influenzae*, *Helicobacter pylori* 26695, *Helicobacter pylori* J99, *Methanobacterium thermoautotrophicum*, *Methanococcus jannaschii*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Pseudomonas aeruginosa*, *Pyrococcus abyssi*, *Pyrococcus horikoshii*, *Rickettsia prowazekii*, *Synechocystis* PCC6803, *Thermotoga maritima*, *Treponema pallidum*, *Bordetella pertussis*, *Campylobacter jejuni*, *Clostridium acetobutylicum*, *Mycobacterium tuberculosis* CSU#93, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pseudomonas aeruginosa*, *Pyrobaculum aerophilum*, *Pyrococcus furiosus*, *Rhodobacter capsulatus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Ureaplasma urealyticum* and *Vibrio cholera* are available. This nucleotide sequence information is stored in a number of databanks, such as GenBank, the National Center for Biotechnology Information (NCBI), the Genome Sequencing Center (<http://genome.wustl.edu/gsc/salmonella.shtml>), and the Sanger Centre (http://www.sanger.ac.uk/projects/S_typhi) which are publicly available for searching.

Please replace the paragraph spanning pages 123-124 with the following:

The nucleotide sequences of the subcloned fragments from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* obtained from the expression vectors discussed above were compared to known sequences from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas*

aeruginosa or *Enterococcus faecalis* and other microorganisms as follows. First, to confirm that each clone originated from one location on the chromosome and was not chimeric, the nucleotide sequences of the selected clones were compared against the *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* genomic sequences to align the clone to the correct position on the chromosome. The NCBI BLASTN v 2.0.9 program was used for this comparison, and the incomplete *Staphylococcus aureus* genomic sequences licensed from TIGR, as well as the NCBI nonredundant GenBank database were used as the source of genomic data. *Salmonella typhimurium* sequences were compared to sequences available from the Genome Sequencing Center (<http://genome.wustl.edu/gsc/salmonella.shtml>), and the Sanger Centre (http://www.sanger.ac.uk/projects/S_typhi). *Pseudomonas aeruginosa* sequences were compared to a proprietary database and the NCBI GenBank database. The *E. faecalis* sequences were compared to a proprietary database.

Please replace the paragraph spanning pages 125-126 with the following:

Alternatively, ORFs were identified and refined by conducting a survey of the public and private data sources. Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Pseudomonas aeruginosa*, gene sequences were adopted from the *Pseudomonas* genome sequencing project (~~downloaded from~~ <http://www.pseudomonas.com>). For *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Salmonella typhi*, genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.

Please replace the second full paragraph on page 127 with the following:

Operons are predicted by looking for all adjacent genes in a genomic region that lie in the same orientation with no large noncoding gaps in between. First, full-length ORFs

complementary to the antisense molecules are identified as described above. Adjacent ORFs are then identified and their relative orientation determined either by directly analyzing the genomic sequences surrounding the ORFs complementary to the antisense clones or by extracting adjacent ORFs from the collection obtained through whole genome ORF analysis described above followed by ORF alignment. Operons predicted in this way may be confirmed by comparison to the arrangement of the homologous nucleic acids in the *Bacillus subtilis* complete genome sequence, as reported by the genome database compiled at Institut Pasteur Subtilist Release R15.1 (June 24, 1999) which can be found at <http://bioweb.pasteur.fr/GenoList/Subtilist/>. The *Bacillus subtilis* genome is the only fully sequenced and annotated genome from a Gram-positive microorganism, and appears to have a high level of similarity to *Staphylococcus aureus* both at the level of conservation of gene sequence and genomic organization including operon structure. Operons for *Salmonella typhimurium* and *Klebsiella pneumoniae* may be identified by comparison with *E. coli*, *Haemophilus*, or *Pseudomonas* sequences. The *Pseudomonas aeruginosa* web site (<http://www.pseudomonas.com>) can also be used to help predict operon organization in this bacterium.